

Official, please enter.

Malicka

20

25

30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
35 40

<210> 32
<211> 262
<212> DNA
<213> Homo sapiens

<220>
<223> Intron X. Complete length unknown

<400> 32
gacagtccacc aggggggttg accgcggac tggcggtccc cagggttgac tataggacca 60
ggtgtccagg tgcctgcga gttagagggc ttcagagggc gtctggctgg catgggtgg 120
cgtggccccg ggcattggcct tctgcgtgtg ctgcgtggg tgcctgtggc cctcaactgag 180
tcgggtggggg cttgtggctt cccgtgagct tccttcctat ctgttgtctg gctgagcaag 240
cctcctgagg ggctctctat tg 262

<210> 33
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33
gtggctgtgc ttgggttaa cttcctttt aaccagaagt ggtttgagc cccacatttg 60
gtatcagtt agatgaaggg cccggaggag gggccacggg acacagccag ggcctatggca 120
cggcgcacccac ccatttgcgc gcacagttagt gtggccgagg tgccggtgcc tccagaaaaag 180
cagcgtggggg gtgttaggggg agtcctggg gcaggggac 218

<210> 34
<211> 2031
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1767)..(1769)
<223> Wherein N is A, C, G or T

<220>
<223> Truncated Telomerase

<400> 34
atgccgcgcg ctccccgcgtg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgcgcg tggcacgtt cgtgcggcgc ctggggccccc agggctggcg gctgggtgcag 120
cgccgggaccc cggcggtttt ccgcgcgtg gtggcccaagt gcctgggttg cgtgcctgg 180
gacgcacggc cgccccccgc cgccttc ttcgcgcagg tgcctgcct gaaggagctg 240
gtggcccgag tgcgtgcagag gctgtgcgag cggcgccgca agaacgtgtc ggccttcggc 300
ttcgcgtgc tggacggggc ccgcggggc ccccccgggg cttcaccac cagegtgcgc 360
agctacactgc ccaacacggc gaccgacgcgca ctgcggggga gcggggcgtg ggggctgtg 420
ctgcgcgcg tggcgacga cgtgcgtgtt cacctgtgtg cacgctgcgc gctctttgtg 480

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
 1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
 1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 1075 1080

<210> 51

<211> 2135

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1871)..(1873)

<223> Wherein N is A, C, G or T

<220>

<223> Truncated Telomerase (ver. 2); with
 Intron Y

<400> 51

atgccgcgctg ctccccgtg ccgagccgtg cgctccctgc tgcgcaagcca ctaccgcgag 60
 gtgctgccgc tgccacgtt cgtgcggcgc ctggggccccc agggctggcg gctggtgtcag 120
 cgcggggacc cggcggttt ccgcgcgtg gtggcccaagt gcctgggtgtg cgtgcctgg 180
 gacgcacggc cgcggggccgc cgcggggccgc ttccgcccagg tgggcctccc cggggtcggc 240
 gtccggctgg gtttggggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
 gactcagggc gttcccccg caggtgttct gcctgaagga gctggtgccc cgagtgtcgc 360
 agaggctgtg cgagcgccgc gcgaagaacg tgcgtggcctt cggcttcgcgc ctgctggacg 420
 gggcccgccgg gggccggccgc gaggccttca ccaccagcgt ggcgcagctac ctgcggaaaca 480
 cggtgaccga cgaactgcgg gggagcgggg cgtgggggtt gctgtgcgc cgctggggcg 540
 acgacgtgtt gttcacctg ctggcacgtt gegegotctt tgtgtggtg gctcccagct 600
 ggccttacca ggtgtgcggg cgcggctgtt accagctcgg cgctgcact caggccggc 660
 ccccgccaca cgttagtggc ccccgaaaggc gtctggatg cgaacgggc tgaaccata 720
 gcgtcaggga ggcgggggtc cccctggcc tggcagcccc ggtgtcgagg aggcgcgggg 780
 gcagtgccag ccgaagtctg ccgttgcucca agaggcccag gcgtggcgct gcccctgagc 840
 cggagccggac gcccgttggg caggggttct gggcccaccc gggcaggacg cgctggaccga 900
 gtgaccgtgg ttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acccttttg 960
 agggtgcgtt ctctggcacg cgccactccc acccatecgt gggccggccag caccacgcgg 1020
 gccccccatc cacatgcgg ccaccacgtc cctgggacac gcctgtccc ccggtgtacg 1080
 ccgagaccaa gcacttcctc tactcctcag gcgacaaggc gcagctgcgg cccttccttc 1140
 tactcagctc tctgaggccc agcctgactg gcgcgtcgag gctctggag accattttc 1200
 tgggttccag gcctggatg ccaggactc cccgcagggtt gccccgcctg ccccagcgct 1260
 actggcaaatt gcccggccctg ttctgtgagc tgcttggaa ccacgcgcag tgcccctacg 1320
 ggggtgttctt caagacgcac tgccgcgtgc gagctgcggc caccgcac gcccgtgtct 1380
 gtgcccggga gaagccccag ggtctgtgg cggcccccga ggaggaggac acagaccccc 1440
 gtcgcctgtt gcagctgttc cgcgcacaca gcagccccctg gcaggtgtac ggcttcgtgc 1500
 gggcctgcct gcccggcgctg gtgccccccag gcctctgggg ctccaggcac aacgaacgc 1560
 gttccctcag gaacaccaag aagtccatct ccctggggaa gcatgcacag ctctcgctgc 1620
 aggagctgac gtggaaagatg agcgtgcggg actgcgttgc gctgcgcagg agcccagggg 1680
 ttggctgtgt tccggccgc gaggcaccgtc tgctgtgagga gatccctggcc aagtccctgc 1740
 actggctgtat gagttgtgtac gtctgcgcgc tgctcagggtc ttcttttat gtacggaga 1800
 ccacgtttca aaagaacagg ctcttttctt accggaaagag tgcgtggagc aagttgaaaa 1860
 gcattggaat nnngacagtc accagggggg ttgaccgcgc gactggcggtt ccccgagggtt 1920

gactatagga ccagggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
 tggcatgggt ggacgtggcc cccggcatgg cttctgcgt gtgtcgccgt ggggtgccttg 2040
 agccctcaact gagtcgggtgg gggcttgtgg ctccccgtga gttccccct agtctgttgt 2100
 ctggctgagc aaggctcctg aggggctctc tattg 2135

<210> 52
 <211> 622
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Truncated Telomerase (ver.2); encoded
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser
1									10					15	

His	Tyr	Arg	Glu	VaL	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
				20					25				30		

Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg
							35	40				45			

Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro
						50	55			60					

Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Gly	Leu	Pro	Gly	Val	Gly
						65	70		75		80				

Val	Arg	Leu	Gly	Leu	Arg	Ala	Ala	Gly	Gly	Asn	Gln	Arg	His	Ala	Glu
						85		90			95				

Ser	Ser	Ala	Gly	Asp	Ser	Gly	Arg	Phe	Pro	Arg	Arg	Ser	Cys	Leu	Lys
							100	105			110				

Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
						115	120		125						

Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly
						130	135		140						

Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr
						145	150		155		160				

Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Arg
						165		170		175				

Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu
						180		185		190					

Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
						195	200		205						

Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
						210	215		220						

Ser	Gly	Pro	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

225	230	235	240
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg			
245	250	255	
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro			
260	265	270	
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly			
275	280	285	
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe			
290	295	300	
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu			
305	310	315	320
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln			
325	330	335	
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp			
340	345	350	
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser			
355	360	365	
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu			370
375	380		
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu			
385	390	395	400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu			
405	410	415	
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly			
420	425	430	
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro			
435	440	445	
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys			
450	455	460	
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg			
465	470	475	480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr			
485	490	495	
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp			
500	505	510	
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe			
515	520	525	
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp			
530	535	540	

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val
545 550 555 560
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala
565 570 575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg
580 585 590
Ser Phe Phe Tyr Val Thr Glu Thr Phe Gln Lys Asn Arg Leu Phe
595 600 605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
610 615 620

<210> 53
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<223> Splicing Variant of Human Telomerase encoded by
Intron Y, ORF2, before the termination codon.
SEQ ID NOS: 51,55,59,63,67,71,75,79,83 encode this
fragment

<400> 53
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala
65 70 75 80

Ser Gly Trp Gly

<210> 54
<211> 537
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<210> 154
<211> 4
<212> PRT
<213> Homo sapiens

<400> 154
Arg Ala Thr Ser
1

<210> 155
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<223> Truncated Telomerase (ver.2); encoded
by SEQ ID NO:51, with Y Intron ORF3

<400> 155
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro